In the specification:

Please replace Table 1 at page 9 of the specification with the following amended Table 1:

Table I

Positions in the RSL which can be changed

POSITION IN THE REACTIVE SITE LOOP

P5	P4	P3	P2	P1	P*1	P*2	P*3	P*4	SEQ ID NO:
		S	S	R	T	E			23
		K	T	R	S	N			24
	I	S	P	R	S				25
	G	V	F	R	S				26
	G	T	V	R	S				27
	E	T	K	R	S				28
		L	G	R	S	L			29
		R	G	R	S	E			30
			R	R	S	I	D		31
		V	L	R	S	P			32
		P	F	R	S	S			33
				R	S	G	S	V	34
	A	R	A	R	S				35
		S	D	R	T	A			36
		K	L	R	T	T			37
				R	A	A	M	M	38
				R	A	P	M		39
		D	V	R	A	A			40
		P	G	R	A	P			41
	V	E	S	R	A				42
			A	R	A	S	E		43
	T	L	Q	R	V				44
	R	L	E	R	V				45
			E	R	V	S	P		46
	S	S	P	R	V				47
				R	V	G	P	Y	48
	P	S	A	R	M				49
		R	G	R	M	A			50
		T	V	R	M	P			51
			L	R	M	P	T		52
			H	R	M	S	S		53
				R	P	Q	E	L	54
			V	R	P	L	E		55
		S	G	R	L	A			56
	G	T	L	R	F				57
		Q	W	R	N	S			58
				R	N	D	K	L	59
			M	R	N	R	A		60

								SEQ ID NO
			T	R	D	S	R	<u>61</u>
	T	G	S	R	D			<u>62</u>
	I	M	S	R	Q			<u>63</u>
	E	Q	H	R	Q	M	G	<u>64</u>
L	T	T	S	K				<u>65</u>
	P	F	R	K	I			<u>66</u>
		<u>M</u>	<u>T</u>	<u>R</u>	<u>S</u>	<u>N</u>		<u>67</u>
		<u>L</u>	<u>R</u>	<u>S</u>	<u>R</u>	<u>A</u>		<u>68</u>

Amino acid sequence of P4-P3' residues in RSL (Reactive Serpin Loop) corresponding to potential substrate peptide

Blank spaces indicate that there is no modification needed in order to obtain substrate specificity to hK2.

Please replace Table IV at page 9 of the specification with the following amended Table IV:

TABLE IV

Alignment of RSL (Reactive Serpin Loop) of recombinant serpin α1-antichymotrypsin (ACT) and its variants.

Serpin	Selected[a] Substrate Peptide	P6	P5	P4	P3	P2	*P1*	P'1	P'2	P'3	P'4	P'5	P'6	SEQ ID NO
rACT$_{WT}$		V	K	I	T	L	*L**	S	A	L	V	E	T	<u>15</u>
rACT$_{8.20}$	LR↓SRA	V	K	I	T	<u>**L**</u>	**R***	S	<u>**R**</u>	<u>**A**</u>	V	E	T	<u>16</u>
rACT$_{6.2}$	RR↓SID	V	K	I	T	<u>**R**</u>	**R***	S	<u>**I**</u>	<u>**D**</u>	V	E	T	<u>17</u>
rACT$_{8.3}$	RGR↓SE	V	K	I	<u>**R**</u>	<u>**G**</u>	**R***	<u>**S**</u>	<u>**E**</u>	L	V	E	T	<u>18</u>
rACT$_{6.7}$	KLR↓TT	V	K	I	<u>**K**</u>	<u>**L**</u>	**R***	<u>**T**</u>	<u>**T**</u>	L	V	E	T	<u>19</u>
rACT$_{6.1}$	MTR↓SN	V	K	I	<u>**M**</u>	<u>**T**</u>	**R***	<u>**S**</u>	<u>**N**</u>	<u>**A**</u>	V	E	T	<u>20</u>
ACT$_{5.18}$	ER↓VSP	V	K	I	T	<u>**E**</u>	**R***	<u>**V**</u>	<u>**S**</u>	<u>**P**</u>	V	E	T	<u>21</u>

[a] Substrate peptides selected by kallikrein hK2 using a phage-displayed random pentapeptide library .

Plain type residues are common to rACT$_{WT}$, bold and underlined residues correspond to substrate peptides relocated in RSL of ACT variants. The scissile bond by hK2 in substrate peptides is designated by ↓ and putative cleavage site in serpins is marked by asterisks between the P1-P1' residues.